

1

SEQUENCE LISTING

<110> Teem, John L.

<120> Materials and Methods for Detecting Interaction of CFTR Polypeptides

<130> FSU-100XC1

<140> (not yet assigned)

<141> 2000-10-06

<150> 60/157,996

<151> 1999-10-06

<150> 60/181,892

<151> 2000-02-11

<150> 60/182,373

<151> 2000-02-14

<160> 4

<170> PatentIn version 3.0

<210> 1

<211> 25

<212> DNA

<213> Homo sapien

<400> 1

cgcggaattc actcggcaat ttccc

2

<210> 2

<211> 28

<212> DNA

<213> Homo sapien

<400> 2

gcgcctgcag ttaagaacag aatgaaat

28

<210> 3

<211> 4443

<212> DNA

<213> Homo sapien

<220>

<221> gene

<222> (1) .. (4443)

<400> 3

atgcagaggt cgcctctgga aaaggccagc gttgtctcca aacttttttt cagctggacc 60

agaccaatth tgaggaaagg atacagacag cgcctggaat tgcagacat ataccaaatc 120

ccttctgttg attctgctga caatctatct gaaaaattgg aaagagaatg ggatagagag 180

ctggcttcaa agaaaaatcc taaactcatt aatgcccttc ggcgatgttt tttctggaga 240

tttatgttct atggaatctt tttatathta ggggaagtca ccaaagcagt acagcctctc 300

ttactgggaa gaatcatagc ttcctatgac ccggataaca aggaggaacg ctctatcgcg 360

atttatctag gcataggctt atgccttctc tttattgtga ggacactgct cctacaccca 420
gccatttttg gccttcatca cattggaatg cagatgagaa tagctatggt tagtttgatt 480
tataagaaga ctttaaagct gtcaagccgt gttctagata aaataagtat tggacaactt 540
gttagtctcc tttccaacaa cctgaacaaa tttgatgaag gacttgcatt ggcacatttc 600
gtgtggatcg ctcttttgca agtggcactc ctcatggggc taatctggga gttgttacag 660
gcgtctgcct tctgtggact tggtttcctg atagtccttg ccctttttca ggctgggcta 720
gggagaatga tgatgaagta cagagatcag agagctggga agatcagtga aagacttgtg 780
attacctcag aaatgattga aaatatccaa tctgttaagg catactgctg ggaagaagca 840
atggaaaaaa tgattgaaaa cttaagacaa acagaactga aactgactcg gaaggcagcc 900
tatgtgagat acttcaatag ctcagccttc ttcttctcag ggttctttgt ggtgttttta 960
tctgtgcttc cctatgcact aatcaaagga atcatcctcc ggaaaatatt caccaccatc 1020
tcattctgca ttgttctgcg catggcggtc actcggcaat ttccctgggc tgtacaaaca 1080
tggtatgact ctcttgagc aataaacaaa atacaggatt tcttacaaaa gcaagaatat 1140
aagacattgg aatataactt aacgactaca gaagtagtga tggagaatgt aacagccttc 1200
tgggaggagg gatttgggga attatttgag aaagcaaac aaaacaataa caatagaaaa 1260
acttctaatz gtgatgacag cctcttcttc agtaatttct cacttcttgg tactcctgtc 1320
ctgaaagata ttaatttcaa gatagaaaga ggacagttgt tggcggttgc tggatccact 1380
ggagcaggca agacttcact tctaatzatg attatgggag aactggagcc ttcagagggt 1440
aaaattaagc acagtggag aatttcattc tgttctcagt tttcttgat tatgcctggc 1500
accattaaag aaaatatcat ctttggtggt tcctatzatg aatatagata cagaagcgtc 1560
atcaaagcat gccaaactaga agaggacatc tccaagtttg cagagaaaga caatatagtt 1620

cttggagaag gtggaatcac actgagtgga ggtcaacgag caagaatttc ttagcaaga 1680
gcagtataca aagatgctga tttgtattta ttagactctc cttttggata cctagatgtt 1740
ttaacagaaa aagaaatatt tgaaagctgt gtctgtaaac tgatggctaa caaaactagg 1800
attttgggtca cttctaaaat ggaacattta aagaaagctg acaaaatatt aattttgcat 1860
gaaggtagca gctattttta tgggacattt tcagaactcc aaaatctaca gccagacttt 1920
agctcaaaac tcatgggatg tgattctttc gaccaattta gtgcagaaag aagaaattca 1980
atcctaactg agaccttaca ccgtttctca ttagaaggag atgctcctgt ctctggaca 2040
gaaacaaaaa aacaatcttt taaacagact ggagagtttg gggaaaaaag gaagaattct 2100
attctcaatc caatcaactc tatacgaana ttttccattg tgcaaaagac tcccttaca 2160
atgaatggca tcgaagagga ttctgatgag cctttagaga gaaggctgtc cttagtacca 2220
gattctgagc agggagaggc gatactgcct cgcacagcg tgatcagcac tggccccacg 2280
cttcaggcac gaaggaggca gtctgtcctg aacctgatga cacactcagt taaccaaggt 2340
cagaacattc accgaaagac aacagcatcc acacgaaaag tgtcactggc cctcaggca 2400
aacttgactg aactggatat atattcaaga aggttatctc aagaaactgg cttggaaata 2460
agtgaagaaa ttaacgaaga agacttaaag gagtgctttt ttgatgatat ggagagcata 2520
ccagcagtga ctacatggaa cacatacctt cgatatatta ctgtccacaa gagcttaatt 2580
tttgtgctaa tttgggtgctt agtaattttt ctggcagagg tggctgcttc tttggttggtg 2640
ctgtggctcc ttggaaacac tcctcttcaa gacaaaggga atagtactca tagtagaaat 2700
aacagctatg cagtgattat caccagcacc agttcgtatt atgtgtttta catttacgtg 2760
ggagtagccg acactttgct tgctatggga ttcttcagag gtctaccact ggtgcatact 2820
ctaatacag tgtcgaaaat ttacaccac aaaatgttac attctgttct tcaagcacct 2880

atgtcaaccc tcaacacgtt gaaagcaggt gggattctta atagattctc caaagatata 2940
gcaattttgg atgaccttct gcctcttacc atatttgact tcatccagtt gttattaatt 3000
gtgattggag ctatagcagt tgtcgcagtt ttacaaccct acatctttgt tgcaacagtg 3060
ccagtgatag tggcttttat tatgttgaga gcatatttcc tccaaacctc acagcaactc 3120
aaacaactgg aatctgaagg caggagtcca attttctact atcttgttac aagcttaaaa 3180
ggactatgga cacttcgtgc cttcggacgg cagccttact ttgaaactct gttccacaaa 3240
gctctgaatt tacatactgc caactgggtc ttgtacctgt caacactgcg ctgggttccaa 3300
atgagaatag aaatgatatt tgatcatctc ttcatgtctg ttaccttcat ttccatttta 3360
acaacaggag aaggagaagg aagagttggt attatcctga ctttagccat gaatatcatg 3420
agtacattgc agtgggctgt aaactccagc atagatgtgg atagcttgat gcgatctgtg 3480
agccgagtct ttaagttcat tgacatgcca acagaaggta aacctaccaa gtcaacacaaa 3540
ccatacaaga atggccaact ctcgaaagtt atgattattg agaattcaca cgtgaagaaa 3600
gatgacatct ggccctcagg gggccaaatg actgtcaaag atctcacagc aaaatacaca 3660
gaaggtggaa atgccatatt agagaacatt tccttctcaa taagtcctgg ccagaggggtg 3720
ggcctcttgg gaagaactgg atcaggggaag agtactttgt tatcagcttt ttgagacta 3780
ctgaacactg aaggagaaat ccagatcgat ggtgtgtctt gggattcaat aactttgcaa 3840
cagtggagga aagccttttg agtgatacca cagaaagtat ttattttttc tggaacattt 3900
agaaaaaact tggatcccta tgaacagtgg agtgatcaag aaatatggaa agttgcagat 3960
gaggttgggc tcagatctgt gatagaacag tttcctggga agcttgactt tgtccttgtg 4020
gatgggggct gtgtcctaag ccatggccac aagcagttga tgtgcttggc tagatctgtt 4080
ctcagtaagg cgaagatctt gctgcttgat gaaccagtg ctcatattga tccagtaaca 4140

6

taccaaataa ttagaagaac tctaaaacaa gcatttgctg attgcacagt aattctctgt 4200
gaacacagga tagaagcaat gctggaatgc caacaatttt tggatcataga agagaacaaa 4260
gtgcggcagt acgattccat ccagaaactg ctgaacgaga ggagcctctt ccggcaagcc 4320
atcagcccct ccgacagggt gaagctcttt cccacacgga actcaagcaa gtgcaagtct 4380
aagccccaga ttgctgctct gaaagaggag acagaagaag aggtgcaaga tacaaggctt 4440
tag 4443

<210> 4

<211> 1480

<212> PRT

<213> Homo sapien

<220>

<221> PEPTIDE

<222> (1)..(1480)

<400> 4

Met	Gln	Arg	Ser	Pro	Leu	Glu	Lys	Ala	Ser	Val	Val	Ser	Lys	Leu	Phe
1				5				10					15		
Phe	Ser	Trp	Thr	Arg	Pro	Ile	Leu	Arg	Lys	Gly	Tyr	Arg	Gln	Arg	Leu
			20					25					30		
Glu	Leu	Ser	Asp	Ile	Tyr	Gln	Ile	Pro	Ser	Val	Asp	Ser	Ala	Asp	Asn
		35					40					45			
Leu	Ser	Glu	Lys	Leu	Glu	Arg	Glu	Trp	Asp	Arg	Glu	Leu	Ala	Ser	Lys
		50				55					60				

Lys Asn Pro Lys Leu Ile Asn Ala Leu Arg Arg Cys Phe Phe Trp Arg
 65 70 75 80

Phe Met Phe Tyr Gly Ile Phe Leu Tyr Leu Gly Glu Val Thr Lys Ala
 85 90 95

Val Gln Pro Leu Leu Leu Gly Arg Ile Ile Ala Ser Tyr Asp Pro Asp
 100 105 110

Asn Lys Glu Glu Arg Ser Ile Ala Ile Tyr Leu Gly Ile Gly Leu Cys
 115 120 125

Leu Leu Phe Ile Val Arg Thr Leu Leu Leu His Pro Ala Ile Phe Gly
 130 135 140

Leu His His Ile Gly Met Gln Met Arg Ile Ala Met Phe Ser Leu Ile
 145 150 155 160

Tyr Lys Lys Thr Leu Lys Leu Ser Ser Arg Val Leu Asp Lys Ile Ser
 165 170 175

Ile Gly Gln Leu Val Ser Leu Leu Ser Asn Asn Leu Asn Lys Phe Asp
 180 185 190

Glu Gly Leu Ala Leu Ala His Phe Val Trp Ile Ala Pro Leu Gln Val
 195 200 205

Ala Leu Leu Met Gly Leu Ile Trp Glu Leu Leu Gln Ala Ser Ala Phe
 210 215 220

Cys Gly Leu Gly Phe Leu Ile Val Leu Ala Leu Phe Gln Ala Gly Leu
 225 230 235 240

Gly Arg Met Met Met Lys Tyr Arg Asp Gln Arg Ala Gly Lys Ile Ser
 245 250 255

Glu Arg Leu Val Ile Thr Ser Glu Met Ile Glu Asn Ile Gln Ser Val
 260 265 270

8

Lys Ala Tyr Cys Trp Glu Glu Ala Met Glu Lys Met Ile Glu Asn Leu
 275 280 285

Arg Gln Thr Glu Leu Lys Leu Thr Arg Lys Ala Ala Tyr Val Arg Tyr
 290 295 300

Phe Asn Ser Ser Ala Phe Phe Phe Ser Gly Phe Phe Val Val Phe Leu
 305 310 315 320

Ser Val Leu Pro Tyr Ala Leu Ile Lys Gly Ile Ile Leu Arg Lys Ile
 325 330 335

Phe Thr Thr Ile Ser Phe Cys Ile Val Leu Arg Met Ala Val Thr Arg
 340 345 350

Gln Phe Pro Trp Ala Val Gln Thr Trp Tyr Asp Ser Leu Gly Ala Ile
 355 360 365

Asn Lys Ile Gln Asp Phe Leu Gln Lys Gln Glu Tyr Lys Thr Leu Glu
 370 375 380

Tyr Asn Leu Thr Thr Thr Glu Val Val Met Glu Asn Val Thr Ala Phe
 385 390 395 400

Trp Glu Glu Gly Phe Gly Glu Leu Phe Glu Lys Ala Lys Gln Asn Asn
 405 410 415

Asn Asn Arg Lys Thr Ser Asn Gly Asp Asp Ser Leu Phe Phe Ser Asn
 420 425 430

Phe Ser Leu Leu Gly Thr Pro Val Leu Lys Asp Ile Asn Phe Lys Ile
 435 440 445

Glu Arg Gly Gln Leu Leu Ala Val Ala Gly Ser Thr Gly Ala Gly Lys
 450 455 460

Thr Ser Leu Leu Met Met Ile Met Gly Glu Leu Glu Pro Ser Glu Gly
 465 470 475 480

Lys Ile Lys His Ser Gly Arg Ile Ser Phe Cys Ser Gln Phe Ser Trp
485 490 495

Ile Met Pro Gly Thr Ile Lys Glu Asn Ile Ile Phe Gly Val Ser Tyr
500 505 510

Asp Glu Tyr Arg Tyr Arg Ser Val Ile Lys Ala Cys Gln Leu Glu Glu
515 520 525

Asp Ile Ser Lys Phe Ala Glu Lys Asp Asn Ile Val Leu Gly Glu Gly
530 535 540

Gly Ile Thr Leu Ser Gly Gly Gln Arg Ala Arg Ile Ser Leu Ala Arg
545 550 555 560

Ala Val Tyr Lys Asp Ala Asp Leu Tyr Leu Leu Asp Ser Pro Phe Gly
565 570 575

Tyr Leu Asp Val Leu Thr Glu Lys Glu Ile Phe Glu Ser Cys Val Cys
580 585 590

Lys Leu Met Ala Asn Lys Thr Arg Ile Leu Val Thr Ser Lys Met Glu
595 600 605

His Leu Lys Lys Ala Asp Lys Ile Leu Ile Leu His Glu Gly Ser Ser
610 615 620

Tyr Phe Tyr Gly Thr Phe Ser Glu Leu Gln Asn Leu Gln Pro Asp Phe
625 630 635 640

Ser Ser Lys Leu Met Gly Cys Asp Ser Phe Asp Gln Phe Ser Ala Glu
645 650 655

Arg Arg Asn Ser Ile Leu Thr Glu Thr Leu His Arg Phe Ser Leu Glu
660 665 670

Gly Asp Ala Pro Val Ser Trp Thr Glu Thr Lys Lys Gln Ser Phe Lys
675 680 685

10

Gln Thr Gly Glu Phe Gly Glu Lys Arg Lys Asn Ser Ile Leu Asn Pro
 690 695 700

Ile Asn Ser Ile Arg Lys Phe Ser Ile Val Gln Lys Thr Pro Leu Gln
 705 710 715 720

Met Asn Gly Ile Glu Glu Asp Ser Asp Glu Pro Leu Glu Arg Arg Leu
 725 730 735

Ser Leu Val Pro Asp Ser Glu Gln Gly Glu Ala Ile Leu Pro Arg Ile
 740 745 750

Ser Val Ile Ser Thr Gly Pro Thr Leu Gln Ala Arg Arg Arg Gln Ser
 755 760 765

Val Leu Asn Leu Met Thr His Ser Val Asn Gln Gly Gln Asn Ile His
 770 775 780

Arg Lys Thr Thr Ala Ser Thr Arg Lys Val Ser Leu Ala Pro Gln Ala
 785 790 795 800

Asn Leu Thr Glu Leu Asp Ile Tyr Ser Arg Arg Leu Ser Gln Glu Thr
 805 810 815

Gly Leu Glu Ile Ser Glu Glu Ile Asn Glu Glu Asp Leu Lys Glu Cys
 820 825 830

Leu Phe Asp Asp Met Glu Ser Ile Pro Ala Val Thr Thr Trp Asn Thr
 835 840 845

Tyr Leu Arg Tyr Ile Thr Val His Lys Ser Leu Ile Phe Val Leu Ile
 850 855 860

Trp Cys Leu Val Ile Phe Leu Ala Glu Val Ala Ala Ser Leu Val Val
 865 870 875 880

Leu Trp Leu Leu Gly Asn Thr Pro Leu Gln Asp Lys Gly Asn Ser Thr
 885 890 895

His	Ser	Arg	Asn	Asn	Ser	Tyr	Ala	Val	Ile	Ile	Thr	Ser	Thr	Ser	Ser	
			900					905					910			
Tyr	Tyr	Val	Phe	Tyr	Ile	Tyr	Val	Gly	Val	Ala	Asp	Thr	Leu	Leu	Ala	
		915					920					925				
Met	Gly	Phe	Phe	Arg	Gly	Leu	Pro	Leu	Val	His	Thr	Leu	Ile	Thr	Val	
		930				935						940				
Ser	Lys	Ile	Leu	His	His	Lys	Met	Leu	His	Ser	Val	Leu	Gln	Ala	Pro	
945					950					955				960		
Met	Ser	Thr	Leu	Asn	Thr	Leu	Lys	Ala	Gly	Gly	Ile	Leu	Asn	Arg	Phe	
				965					970					975		
Ser	Lys	Asp	Ile	Ala	Ile	Leu	Asp	Asp	Leu	Leu	Pro	Leu	Thr	Ile	Phe	
			980					985					990			
Asp	Phe	Ile	Gln	Leu	Leu	Leu	Ile	Val	Ile	Gly	Ala	Ile	Ala	Val	Val	
		995					1000						1005			
Ala	Val	Leu	Gln	Pro	Tyr	Ile	Phe	Val	Ala	Thr	Val	Pro	Val	Ile	Val	
		1010				1015					1020					
Ala	Phe	Ile	Met	Leu	Arg	Ala	Tyr	Phe	Leu	Gln	Thr	Ser	Gln	Gln	Leu	
1025				1030						1035				1040		
Lys	Gln	Leu	Glu	Ser	Glu	Gly	Arg	Ser	Pro	Ile	Phe	Thr	His	Leu	Val	
			1045					1050					1055			
Thr	Ser	Leu	Lys	Gly	Leu	Trp	Thr	Leu	Arg	Ala	Phe	Gly	Arg	Gln	Pro	
		1060						1065					1070			
Tyr	Phe	Glu	Thr	Leu	Phe	His	Lys	Ala	Leu	Asn	Leu	His	Thr	Ala	Asn	
		1075				1080						1085				
Trp	Phe	Leu	Tyr	Leu	Ser	Thr	Leu	Arg	Trp	Phe	Gln	Met	Arg	Ile	Glu	
		1090				1095					1100					

12

Met Ile Phe Val Ile Phe Phe Ile Ala Val Thr Phe Ile Ser Ile Leu
1105 1110 1115 1120

Thr Thr Gly Glu Gly Glu Gly Arg Val Gly Ile Ile Leu Thr Leu Ala
1125 1130 1135

Met Asn Ile Met Ser Thr Leu Gln Trp Ala Val Asn Ser Ser Ile Asp
1140 1145 1150

Val Asp Ser Leu Met Arg Ser Val Ser Arg Val Phe Lys Phe Ile Asp
1155 1160 1165

Met Pro Thr Glu Gly Lys Pro Thr Lys Ser Thr Lys Pro Tyr Lys Asn
1170 1175 1180

Gly Gln Leu Ser Lys Val Met Ile Ile Glu Asn Ser His Val Lys Lys
1185 1190 1195 1200

Asp Asp Ile Trp Pro Ser Gly Gly Gln Met Thr Val Lys Asp Leu Thr
1205 1210 1215

Ala Lys Tyr Thr Glu Gly Gly Asn Ala Ile Leu Glu Asn Ile Ser Phe
1220 1225 1230

Ser Ile Ser Pro Gly Gln Arg Val Gly Leu Leu Gly Arg Thr Gly Ser
1235 1240 1245

Gly Lys Ser Thr Leu Leu Ser Ala Phe Leu Arg Leu Leu Asn Thr Glu
1250 1255 1260

Gly Glu Ile Gln Ile Asp Gly Val Ser Trp Asp Ser Ile Thr Leu Gln
1265 1270 1275 1280

Gln Trp Arg Lys Ala Phe Gly Val Ile Pro Gln Lys Val Phe Ile Phe
1285 1290 1295

Ser Gly Thr Phe Arg Lys Asn Leu Asp Pro Tyr Glu Gln Trp Ser Asp
1300 1305 1310

13

Gln Glu Ile Trp Lys Val Ala Asp Glu Val Gly Leu Arg Ser Val Ile
1315 1320 1325

Glu Gln Phe Pro Gly Lys Leu Asp Phe Val Leu Val Asp Gly Gly Cys
1330 1335 1340

Val Leu Ser His Gly His Lys Gln Leu Met Cys Leu Ala Arg Ser Val
1345 1350 1355 1360

Leu Ser Lys Ala Lys Ile Leu Leu Leu Asp Glu Pro Ser Ala His Leu
1365 1370 1375

Asp Pro Val Thr Tyr Gln Ile Ile Arg Arg Thr Leu Lys Gln Ala Phe
1380 1385 1390

Ala Asp Cys Thr Val Ile Leu Cys Glu His Arg Ile Glu Ala Met Leu
1395 1400 1405

Glu Cys Gln Gln Phe Leu Val Ile Glu Glu Asn Lys Val Arg Gln Tyr
1410 1415 1420

Asp Ser Ile Gln Lys Leu Leu Asn Glu Arg Ser Leu Phe Arg Gln Ala
1425 1430 1435 1440

Ile Ser Pro Ser Asp Arg Val Lys Leu Phe Pro His Arg Asn Ser Ser
1445 1450 1455

Lys Cys Lys Ser Lys Pro Gln Ile Ala Ala Leu Lys Glu Glu Thr Glu
1460 1465 1470

Glu Glu Val Gln Asp Thr Arg Leu
1475 1480